

Amendments to the Specification

Please replace the title at page 1, line 6, with the following amended title:

METHODS FOR IDENTIFYING COMPOUNDS THAT MODULATE deltaTRalpha2
ACTIVITY

Please replace the paragraph beginning at page 1, line 8, with the following amended paragraph:

This application is a continuation and claims the benefit of U.S. Patent Application Serial No. 09/894,734, filed on June 28, 2001, now U.S. Pat. No. 6,730,472, issued May 4, 2004, which claims the benefit of U.S. Provisional Patent Application Serial No. 60/214,572, filed on June 28, 2000, both of which are incorporated herein by reference in their entirety.

Please replace the paragraph beginning at page 7, line 17, with the following amended paragraph:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch ((1970) J. Mol. Biol. 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at ~~http://www.gcg.com~~ www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at ~~http://www.gcg.com~~ www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. Another set of parameters (e.g., that can be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or

homology limitation of the invention) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Please replace the paragraph beginning at page 8, line 5, with the following amended paragraph:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences (such as human $\Delta TR\alpha 1$, $\Delta TR\alpha 2$, or myosin V amino acid or nucleic acid sequences). Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to nucleic acid molecules useful in the invention (such as human $\Delta TR\alpha 1$, $\Delta TR\alpha 2$, or myosin V). BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to protein molecules useful in the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov> ~~www.ncbi.nlm.nih.gov~~ www.ncbi.nlm.nih.gov.